Amendments to the Specification

Please replace paragraph **[0164]** of the published application with the following rewritten paragraph:

[0164] In that case where an RNA probe with a 5' splice site has been used in the analytical batch, the oligo-T start primer T_{15} at its anterior 5' end should have another sequence of 18 or more other, alternating nucleotides subsequently serving as recognition sequence for the second primer in the PCR (i.e., total primer length is 33 or more nucleotides) (see Fig. 17C, example: 5'-AACCGGCCAACCGGCCAA-T_{15}-3', SEQ ID NO:1), Using appropriate bioinformatic programs, the sequence of these 18 or more nucleotides must be selected such that self-annealing etc. is avoided. Conceivably, restriction sites (e.g. EcoRI, BamHI etc.) included in said 18-mer sequences might be useful for further work (e.g. cloning); similarly, a nucleotide sequence longer than 18-mer may be convenient (e.g. 36 to 40-mer) to enable a so-called nested PCR (i.e., two different 18 to 20-mer primers undergo binding in a 2-phase PCR) for improved selection (see below).

Please replace paragraph **[0166]** of the published application with the following rewritten paragraph:

[0166] a) In the case of an unknown trans-spliced RNA including the exon portion of an RNA probe with a 5' splice site, synthesis of the second cDNA strand starts in the original region of the exon of the probe RNA. That is, synthesis simply begins with a primer that corresponds to an 18-mer base sequence of the exon of the probe RNA (Fig. 17D, example: 5'-AGAAGAACGGAAGAACAA-3', SEQ ID NO:2). Synthesis of this 2nd strand from the ss-cDNA is effected e.g. by means of a single-cycle PCR or other procedures (see Fig. 17D).

Please replace paragraph **[0168]** of the published application with the following rewritten paragraph:

[0168] For example, advantage can be taken of the fact that the reverse transcriptase, having reached the cap site on the (trans-spliced) mRNA, appends preferably several cytosines to a C chain on the single-stranded cDNA in a terminal transferase function (see Fig. 18C). Moreover, this reaction can be intensified by an excess of cytosines in the substrate compared to the other three substrate nucleotides. This N-terminal cytosine stretch of the ss-cDNA then is used as binding site for a specific primer (cap primer) including in the downstream region thereof a sequence of about 6 to 8 guanosines (G) pairing to the cytosines (see Fig. 18D). The cap primer is added about 30 to 45 minutes after beginning the ss-cDNA synthesis at a temperature lowered to about 30°C. Said specific primer (see example: 5'-GGTTGGAAGGTTGGAAGGGGGG-3', SEQ ID NO:3) in its 18-mer (or longer) sequence upstream of the G nucleotides then is used as a template for further completion with corresponding nucleotides pairing to this primer sequence (see Figs. 18D, 18E). Such completion is effected by the reverse transcriptase or by another suitable DNA polymerase that is added (likewise at about 30 to 32°C). Following heat denaturation to remove this primer from the ss-cDNA, the actual synthesis of the 2^{nd} strand is performed by means of a single-cycle PCR using a primer which has a configuration as the cap primer above but optionally does not include the distal G stretch (see Fig. 18F, example: primer 5'-GGTTGGAAGGTTGGAAG-3', SEQ ID NO:4). In this case as well, it may be convenient to make the region upstream of the oligo-G sequence not only 18 to 20-mer (see Fig. 18C), but rather e.g. 36 to 40-mer in length so as to enable a so-called nested PCR for improved selection (see above, see below). For cloning etc., specific restriction sites (EcoRI, BamHI etc.) can be useful in this primer sequence as well.

Please replace paragraph **[0172]** of the published application with the following rewritten paragraph:

Regarding the batches including a probe RNA with a 5' trans-splice site, the two primers used are as follows: 1) A first primer which binds in the exon portion of the probe RNA and is identical to the primer for the synthesis of the second strand of the ds-cDNA (see example of arbitrary case: 5'-AGAAGAACGGAAGAACAA-3', SEQ ID NO:5, see Figs. 17D, 17K), or a primer which binds downstream of said ds-cDNA primer to the probe RNA exon. If intending to perform a so-called nested PCR (not illustrated in Figs. 17A-17K), the PCR primer of the second PCR correspondingly must bind downstream of the primer of the first PCR in the exon of the probe RNA. 2) The second primer is analogous to the terminal (5') sequence of the 18-21 N-nucleotides of that primer which includes the distal oligo-T portion and is used in the ss-cDNA synthesis (see Fig. 17K, example: 5'-AACCTTCCAACCGGCCAA-3', SEQ ID NO:6). If an approximately 40-mer sequence instead of an 18 to 21-mer sequence upstream of the distal oligo-T portion has been used in the ss-cDNA synthesis, a nested PCR can be performed, wherein the 18 to 21-mer primer of the first PCR corresponds to the 5'-terminal sequence, and the 18 to 21-mer primer of the second PCR corresponds to the 3'-terminal sequence of the above-mentioned 40-mer sequence.

Please replace paragraph **[0173]** of the published application with the following rewritten paragraph:

[0173] Regarding the batches including a probe RNA with a 3' trans-splice site, the primers used are as follows: 1) A first primer which is used in the 2^{nd} strand synthesis of the ds-cDNA (shortened cap primer) (see Fig. 18I, example: 5'-GGTTGGAAGGTTGGAAG-3', SEQ ID NO:4). When using a cap primer with a corresponding overhang sequence of 36 to 40 nucleotides, a so-called nested PCR can be performed subsequently, wherein the 18 to 21-mer primer of the first nested PCR pairs to the 5'-terminal portion of the 36 to 40-mer sequence, and

the 18 to 21-mer primer of the second nested PCR pairs to the 3'-terminal portion of said sequence of 36 to 40 nucleotides. 2) The second PCR primer is analogous to a known sequence of 18 to 24-mer in the exonic portion of the probe RNA or of the DNA encoding said RNA (see Fig. 18I, example: 5'-CTTGTTCTTCCGTTCTTCT-3', SEQ ID NO:8). If a nested PCR is to be performed, the counterprimer of the second nested PCR is a 18 to 21-mer primer likewise analogous to a corresponding exonic sequence of the probe RNA, but pairing downstream of the primer of the first nested PCR to the exon.